

015745-9.ST25.txt
SEQUENCE LISTING

<110> LUKYANOV, SERGI A
SHAGIN, DMITRY A
YANUSHEVICH, YURY G

<120> FLUORESCENT PROTEINS AND CHROMOPROTEINS FROM NON-AEQUOREA
HYDROZOA SPECIES AND METHODS FOR USING SAME

<130> U 015745-9

<140> 10/532,681

<141> 2005-04-26

<160> 22

<170> PatentIn version 3.3

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<211> 784

<212> DNA

<213> phialidium sp

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<212> PRT

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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Glu Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Ile Thr Tyr His Val Thr Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 3
<211> 705
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>

<223> phiYFP-Y1 mutant of the phiYFP

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aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta      180
gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atgggccaga attaaaggat      240
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gacggagtat ttaaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga      360
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cacacccaaa tgaacacacc cattgggtggg ggaccagtcc atgtccctga ataccatcat      600
atgacatacc atgtcactct cagcaaagat gttactgatc acagggataa catgagcttg      660
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<220>
<223> phiYFP-Y1 mutant of the phiYFP

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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20         25         30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35         40         45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50         55         60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65         70         75         80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85         90         95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe

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100

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Thr Tyr His Val Thr Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

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<213> ARTIFICIAL SEQUENCE

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gacggaaact ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360
gtcaaactta atggacaagg atttaagaaa gacggacatg tgcttggaag gaatcttgaa 420
ttcaatttca cacctcattg tctttacatt tggggagatc aggctaataca tggtttgaag 480
tctgctttca aaattcgcca tgagattact ggatcaaaag gagacttcat tgttcgagac 540
cacacccaaa tgaacacacc cattggtggt ggaccagtc atgtccctga aaaccatcat 600

atgagctacc atgtcaagct cagcaaagat gttactgac acagggataa catgagcttg 660
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<210> 6
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<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> phiYFP-M0 mutant of the phiYFP

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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Arg His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

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Val His Val Pro Glu Asn His His Met Ser Tyr His Val Lys Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 7
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<212> DNA
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<213> ARTIFICIAL SEQUENCE

<220>
<223> phiYFP-M1 mutant of the phiYFP

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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
 35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
 50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
 65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
 85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
 100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
 115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
 165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
 180 185 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
 195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
 210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
 225 230

<210> 9
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<220>
 <223> humanized version of the phiYFP-M1

<400> 9

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aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcacctg      180
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<220>
<223> humanized version of the phiYFP-M1

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Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20          25          30

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Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35          40          45

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Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50          55          60

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Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65          70          75          80

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Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
85          90          95

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Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100         105         110

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Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
 115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
 165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
 180 185 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
 195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
 210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
 225 230

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 <212> DNA
 <213> Anthomedusae species

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 ggtgtcaaaa attttacgttc tagaaaattgc agtacggaag aaaaaccgt catacttggt 180
 gcaatgacag aaacatttca gaaaaaattg ccatataagt tagaattgga tggagatggt 240
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 <213> Anthomedusae species

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 20 25 30

Val Ile Leu Gly Ala Met Thr Glu Thr Phe Gln Lys Lys Leu Pro Tyr
 35 40 45

Lys Leu Glu Leu Asp Gly Asp Val Asp Gly Gln Thr Phe Lys Val Ile
 50 55 60

Gly Glu Gly Val Gly Asp Ala Thr Thr Gly Val Ile Glu Gly Lys Tyr
 65 70 75 80

Val Cys Thr Glu Gly Glu Val Pro Ile Ser Trp Val Ser Leu Ile Thr
 85 90 95

Ser Leu Ser Tyr Gly Ala Lys Cys Phe Val Arg Tyr Pro Asn Glu Ile
 100 105 110

Asn Asp Phe Phe Lys Ser Thr Phe Pro Ser Gly Tyr His Gln Glu Arg
 115 120 125

Lys Ile Thr Tyr Glu Asn Asp Gly Val Leu Glu Thr Ala Ala Lys Ile
 130 135 140

Thr Met Glu Ser Gly Ala Ile Val Asn Arg Ile Asn Val Lys Gly Thr
 145 150 155 160

Gly Phe Asp Lys Asp Gly His Val Cys Gln Lys Asn Leu Glu Ser Ser
 165 170 175

Pro Pro Ser Thr Thr Tyr Val Val Pro Glu Gly Glu Gly Ile Arg Ile
180 185 190

Ile Tyr Arg Asn Ile Tyr Pro Thr Lys Asp Gly His Tyr Val Val Ala
195 200 205

Asp Thr Gln Gln Val Asn Arg Pro Ile Arg Ala Gln Gly Thr Ser Ala
210 215 220

Ile Pro Thr Tyr His His Ile Lys Ser Lys Val Asp Leu Ser Thr Asp
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Pro Glu Glu Asn Lys Asp His Ile Ile Ile Lys Glu Thr Asn Cys Ala
245 250 255

Phe Asp Ala Asp Phe Ser
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<210> 13
<211> 1089
<212> DNA
<213> Anthomedusae species

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cattatttca atccgatatg acattcaaga tcttcatcga tggagtgggtg aatgatcaga 180
aattcacgat aatcgcagat ggatcggtcca aattcccca tggtgacttc aacgtgcatg 240
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acggatttca acctgatgga ccaatcatga aagaccagct tgttgatata ctgccaaactg 540
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<210> 14
<211> 232
<212> PRT
<213> Anthomedusae species
<400> 14

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Phe Ile Asp Gly Val Val Asn Asp Gln Lys Phe Thr Ile Ile Ala Asp
20 25 30

Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
35 40 45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
50 55 60

Gln Tyr Gly Glu Pro Phe Phe Ala Lys Tyr Pro Asn Gly Ile Ser His
65 70 75 80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Thr Ile Asp Arg Thr Val
85 90 95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
100 105 110

Asp Gly Thr Cys Val Ile Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
115 120 125

Gln Pro Asp Gly Pro Ile Met Lys Asp Gln Leu Val Asp Ile Leu Pro
130 135 140

Thr Glu Thr His Met Phe Pro His Gly Ser Asn Ala Val Arg Gln Leu
145 150 155 160

Cys Tyr Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
165 170 175

Phe Asp Ser Lys Leu Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
180 185 190

Gly Pro His Phe Val Thr Val Ile Ile Lys Gln Met Lys Asp Thr Ser
195 200 205

Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
 210 215 220

Val Pro Arg Ile Thr Ser Ala Ile
 225 230

<210> 15
 <211> 699
 <212> DNA
 <213> ARTIFICIAL SEQUENCE

<220>
 <223> S3-2 mutant of hm2CP from a hydromedusa 2 of sub-order Anthomedusa

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 gacttcaacg tacatgctgt gtgcgaaacc gggaaactcc caatgtcatg gaaaccatt 180
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<220>
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 20 25 30

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Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
35 40 45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
50 55 60

Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
65 70 75 80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
85 90 95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
100 105 110

Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
115 120 125

Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
130 135 140

Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu
145 150 155 160

Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
165 170 175

Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
180 185 190

Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser
195 200 205

Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
210 215 220

Val Pro Arg Ile Thr Ser Ala Ile
225 230

<210> 17

<211> 705

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> phiYFP-M1G1 mutant, derived from humanized version of the
phiYFP-M1

<400> 17

015745-9.ST25.txt

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<210> 18
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<220>
 <223> phiYFP-M1C1 mutant, derived from humanized version of the
 phiYFP-M1

<400> 18

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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
 20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
 35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
 50 55 60

Ser Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
 65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
 85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
 100 105 110

015745-9.ST25.txt

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
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Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Thr Ala Tyr Leu
225 230

<210> 19
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<220>
<223> phiYFP-M1C1 mutant, derived from humanized version of the

<400> 19
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705

<210> 20
 <211> 234
 <212> PRT
 <213> ARTIFICIAL SEQUENCE

<220>
 <223> phiYFP-M1C1 mutant, derived from humanized version of the
 phiYFP-M1

<400> 20

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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
 20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
 35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
 50 55 60

Ser Trp Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
 65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
 85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
 100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Lys Gly Gln Gly Phe
 115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140

Pro His Tyr Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
 165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
 180 185 190

Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser
 195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Leu
 210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
 225 230

<210> 21
 <211> 699
 <212> DNA
 <213> ARTIFICIAL SEQUENCE

<220>
 <223> humanized version of th S3-2 mutant of hm2cp from a hydromedusa
 2of sub-order Anthomedusae

<400> 21
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<210> 22
 <211> 232
 <212> PRT
 <213> ARTIFICIAL SEQUENCE

<220>
 <223> humanized S3-2 mutant of hm2cp from a hydromedusa 2 of sub-order
 Anthomedusae

<400> 22

Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
 1 5 10 15

Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp
 Page 18

Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
35 40 45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
50 55 60

Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
65 70 75 80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
85 90 95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
100 105 110

Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
115 120 125

Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
130 135 140

Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu
145 150 155 160

Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
165 170 175

Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
180 185 190

Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser
195 200 205

Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
210 215 220

Val Pro Arg Ile Thr Ser Ala Ile
225 230